**AMENDMENTS TO THE CLAIMS:**

The following listing of claims will replace all prior versions and listings of claims in this application.

1-25. (Canceled)

26. (Currently amended) A method of genotyping a subject with respect to a pathological condition, said method comprising contacting a panel of allele specific oligonucleotides immobilized to a solid support covering a mutation in each of the genes connexion 26, pendrin, mitochondrial 12s rRNA and usherin, with a single-stranded form of RNA or DNA from a subject to be tested labeled directly or indirectly with a report molecule, under conditions which comprise hybridization in the presence of 1-4 X SSC at 30-50°C for 15-90 min followed by washing at 30-50°C in the following sequence:

1-4 X SSC/0.05% - 0.4% SDS (1-5 min);

0.1-1 X SSC/0.05% - 0.4% SDS (2-10 min);

0.5 X -5 X SSC (0.5-3 min);

2-8 X SSC/0.05% SDS (0.5-3 min); and

2-8 X SSC/0.05%-2% Tween (0.5-3 min);

~~which~~ wherein said conditions permit hybridization of single-stranded RNA or DNA which is exactly complementary to an immobilized allele specific oligonucleotide, but substantially less or no hybridization of non-complementary single-stranded RNA or DNA molecules.

27. (Previously presented) The method of claim 26, wherein said panel of allele specific oligonucleotides comprise the oligonucleotide as set forth in SEQ ID NO: 1.

28. (New) A method for genotyping a subject with respect to connexin 26, pendrin, mitochrondrial 12S rRNA and usherin, said method comprising contacting an array of allele specific oligonucleotides immobilized to a solid support with a single-stranded form of RNA or DNA from a subject to be tested labeled directly or indirectly with a reporter molecule capable of giving an identifiable signal under conditions which permit hybridization of single stranded RNA or DNA which is exactly complementary to the immobilized allele specific oligonucleotide but

substantially less or no hybridization of non-complementary single-stranded RNA or DNA molecules, and then screening for the presence or absence or level of reporter molecule which provides an indicator of the genetic identity of the single-stranded RNA or DNA molecule which in turn provides the genotype of the subject, wherein said array comprises oligonucleotides that consist of the sequence $[n]_x$-A wherein A is a nucleotide sequence selected from SEQ ID NOs: 33 to 64,

n is one or a range of different nucleotides and

x is the length of the nucleotide sequence [n],

and each of SEQ ID NOs: 33 to 64 is present in said array.

29. (New) The method of Claim 28 wherein the RNA or DNA from the subjects is directly labelled with labelled nucleotides incorporated *via* polymer chain reaction (PCR).

30. (New) The method of Claim 28 wherein the RNA or DNA from the subject is indirectly labeled with labelled nucleotides *via* hybridization of a labelled oligonucleotide to the test RNA or DNA.

31. (New) The method of any one of Claims 28 -30 wherein the subject is selected from human, a non-human primate, a livestock animal, a laboratory test animal, a companion animal and a captured wild animal.

32. (New) The method of Claim 31 wherein the subject is a human.

33. (New) The method of any one of Claims 28-30 wherein the genotyping is associated with a pathological condition which is genetic deafness, a propensity for development of genetic deafness or is associated with genetic deafness.

34. (New) The method of any one of Claims 28-30 wherein said hybridization is performed under differential hybridization conditions which permit differential hybridization between identical nucleotide sequences having at least one mismatch, and the identity of the genotype of the subject is determined by the presence, absence or level of signal from the reporter molecule.

35. (New) The method of any one Claim 28-30 wherein said hybridization conditions comprise hybridization in the presence of 1-4 X SSC at 30-50°C for 15-90 min followed by

washing 30-50°C in the following sequence:

1-4 X SSC/0.05%-0.4% SDS (1-5min);

0.1-1 X SSC/0.05%-0.4% SDS (2-10min);

0.5-5 X SSC (0.5-3min);

2-8 X SSC/0.05% SDS (0.5-3min); and

2.8 X SSC/0.05%-2% Tween (0.5-3min).

36 (New) A method according to Claim 35, wherein a genotype index (GI) value is determined by the algorithm:-

$$GI = \frac{sv_N}{SV_N ? SV_M}$$

wherein:

$SV_N$ is the normal spot value; and

$SV_M$ is the normal mutant spot value;

such that:

if $0.8 < GI < 1.0$, then the genotype is N/N;

if $0.65 < GI < 0.5$, then the genotype is N/M; and

if $0.0 < GI < 0.2$, then the genotype is M/M;

wherein:

N is a normal allele; and

M is a mutant allele.

37. (New) The method of Claim 36 wherein n is T.

38. (New) The method of Claim 36 wherein x is from about 5 to about 30.

39. (New) The method of Claim 38 wherein x is about 10.

40. (New) The method of any one of Claims 28-30 wherein the array comprises immobilized oligonucleotides with the sequence of SEQ ID NOs: 1 to 32.

41. (New) A set of oligonucleotides having the sequence:

$[n]_x - A$

wherein:

n is one or a range of different nucleotides;

x is the length of the nucleotide sequence [n];

A is a nucleotide sequence selected from SEQ ID NOs: 33 to 64, and

each of SEQ ID NOs 33 to 64 is present in said set.

42. (New) The set of one or more oligonucleotides of Claim 41 wherein n is T.

43. (New) The set of one or more oligonucleotides of Claim 41 wherein x is from about 5 to about 30.

44. (New) The set of oligonucleotides of Claim 41 wherein each oligonucleotide comprises one of SEQ ID NOs: 33 to 64.

45. (New) The set of oligonucleotides of Claim 41 wherein each $[n]_x - A$ is selected from SEQ ID NOs: 1 to 32.

46. (New) An array comprising the set of oligonucleotides of Claim 44 or 45.

47. (New) The array of claim 46, wherein said oligonucleotides are attached to a solid support.